

Result No.	Score	Query Match	Length	DB	ID	Description
1	1248	67.6	1433	1	I37375	death-associated F
2	787	42.6	1435	2	T32930	hypothetical protein
3	703.5	38.1	1176	2	JN0583	myosin-11ght-chain
4	694	37.6	1147	2	A59307	myosin-11ght-chain
5	685.5	37.1	1906	1	S68335	myosin-11ght-chain
6	665.5	36.1	2783	2	T34416	hypothetical protein
7	651.5	35.3	371	2	JC7733	death associated F
8	650	35.2	6658	2	T13931	projectin - fruit
9	621.5	33.7	451	2	S49128	twitchin-like prot
10	605	32.8	608	2	A35021	myosin-11ght-chain
11	604	32.7	610	2	A28798	myosin-11ght-chain
12	589	31.9	1211	2	T27522	hypothetical protein
13	584.5	31.7	6831	2	A88852	protein unc-22 lim
14	584.5	31.7	6839	2	S57242	twitchin (similar)
15	584.5	31.7	7160	2	T27935	hypothetical prote
16	547	29.6	301	1	A40811	myosin-11ght-chain
17	541	29.3	26926	1	I38344	titin, cardiac mus
18	536	29.0	516	1	JU0270	Ca2+/calmodulin-de
19	535	29.0	509	2	B4412	calmodulin-depend
20	534	28.9	530	2	D44412	Ca2+/calmodulin-de
21	532	28.8	474	1	TYRRC4	Ca2+/calmodulin-de
22	532	28.8	502	2	IS2637	Ca2+/calmodulin-de
23	530.5	28.7	370	1	S57947	Ca2+/calmodulin-de
24	530.5	28.7	374	1	S50193	Ca2+/calmodulin-de
25	530	28.7	473	1	A53036	Ca2+/calmodulin-de
26	527.5	28.6	469	1	S17656	Ca2+/calmodulin-de
27	526.5	28.5	533	1	A34366	Ca2+/calmodulin-de
28	510.5	27.7	348	2	T37321	Ca2+/calmodulin-de
29	510	27.6	538	2	T08874	calcium-dependent

30	507.5	27.5	518	1	B46619	Ca2+/calmodulin-de
31	507.5	27.5	556	2	CB5636	Ca2+/calmodulin-de
32	506	27.4	520	2	C84774	probable calcium-d
33	503	27.2	540	1	T01989	calcium-dependent
34	502.5	27.2	484	2	T05650	calcium-dependent
35	502	27.2	527	1	A31908	Ca2+/calmodulin-de
36	500.5	27.1	518	1	S43845	Ca2+/calmodulin-de
37	500.5	27.1	544	2	D84550	probable calmodulin
38	496.5	26.9	573	2	T03940	calcium-dependent
39	493.5	26.7	708	2	T23616	hypothetical prote
40	492.5	26.7	560	2	T46189	calcium-dependent
41	490.5	26.6	533	1	S56652	calcium-dependent
42	488.5	26.5	487	1	S71770	calcium-dependent
43	489.5	26.5	610	1	A43082	calcium-dependent
44	489	26.5	531	2	D85059	probable calcium d
45	488	26.4	520	2	F85059	probable calcium d

ALIGNMENTS

RESULT 1

death-associated protein kinase (EC 2.7.1.-) - human
N:Alternate names: calmodulin-dependent protein kinase homolog; DAP kinase
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 10-Jul-1998
C:Accession: J17275, S39269
R:Delsis, L.P.; Feinstein, E.; Berissi, H.; Cohen, O.; Kimchi, A.
Genes Dev. 9, 15-30, 1995
A:Title: Identification of a novel serine/threonine kinase and a novel 15-kD protein
A:Reference number: A55614, MUID:95129831

A:Molecule type: mRNA
A:Residues: 1-1423 <RES>
A:Cross-references: EMBL:X76104; NID:g434846; PID:g434847
C:Genetics:
A:Gene: GDB:DAPK1; DAPK
A:Cross-references: GDB:555932; OMIM:600831
A:Map position: 9q34.1-9q34.1
A:Function:

A:Description:apoptosis catalyzes the formation of peptidyl-L-serine-phosphate or peptidyl-L-threine
A:Pathway: Apoptosis
A:Note: activity is calmodulin dependent
C:Superfamily: death-associated protein kinase; ankyrin repeat homology; protein kinase
C:Keywords: apoptosis; ATP; calmodulin binding; phosphotransferase; serine/threonine
F:11-267/Domain: protein kinase homology <KIN>
F:19-27/Region: protein kinase ATP-binding motif
F:285-308/Region: calmodulin binding status predicted
F:370-402/Domain: ankyrin repeat homology <AN1>
F:403-435/Domain: ankyrin repeat homology <AN2>
F:436-468/Domain: ankyrin repeat homology <AN3>
F:470-502/Domain: ankyrin repeat homology <AN4>
F:503-535/Domain: ankyrin repeat homology <AN5>
F:536-568/Domain: ankyrin repeat homology <AN6>
F:569-601/Domain: ankyrin repeat homology <AN7>
F:602-634/Domain: ankyrin repeat homology <AN8>
F:42,64,139,141/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 67.68; Score 1248; DB 1; Length 1423;

Matches 236; Conservative 60; Mismatches 43; Indels 16; Gaps 3

QY 1 MEFKQKVEDFYDIGELGSGFAIVKKCREKSTGLEAAKFIKKRQSRASRGVSREE 60

Db 1 MTFVRQENVDDYYDTGEELGSGQFAVVKCKREKSTGLQYPAKFIKKRTKSSRGRVSRD 60

61 IEREVSILRQVLHNVITLHDVYENRTDVHILELVSGGELEFLAQKESLSEEA TSFI 120

Db 61 IEREVSILKEIQHPNVITLHEVYENKTDVILLELVAGGELFDLAEKESLTEEATEFL 120

QY 121 KQILDGVNYLHTKKAHFDLKPENIMLLDKNIPRPHIKLIDGLAHEIEDGVEEFKNIEGT 180


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A:Residues: 1-371 <MAT>
A:Accession: PC7178
A:Molecule type: protein
A:Residues: 227-371 <MA2>
C:Comment: This kinase, a novel calcineurin homologous protein (CHP) binding protein involved in the transfer of Na+/H+ exchange and in some apoptotic events.
C:Genetics:
A:Gene: drak2
C:Keywords: apoptosis

Query Match          35.3%; Score 651.5; DB 2; Length 371;
Best Local Similarity 46.8%; Pred. No. 1.3e-20; Indels 15; Gaps 7;
Matches 133; Conservative 52; Mismatches 84;

3  PRQCKVEPDFYD--GEELSGGQFAIVKCKCEKSTGSLYAKFIKKRQSRASRGVS--REE 60
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
22 PMTEFNENNFTYTPRELGRGKFAAVYRQCLSKSTGGEGYAKFKLR-----RGGQDRAE 76
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 IEREVSIL--ROYLHNVTTLHDVYENKRDVYHIELVSGGELEDFDLAOK--ESLSEE 115
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
77 ILHEIYVLELARSQPH--VNLHEVYETAETVIELVYLAAGGELFNCLDELMEMVSEND 134
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
116 ATSFQIQLDGVNVLHTKTAHFDLKPEPNTMLDKNPIPIHKLIDGLAHEIDSGVEK 175
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
135 VVIRKIRILEGYNHILHQNNTIVHLDLKPQNI--LLSSIVPLDGDKITVDGSMKIGNASLELR 193
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
176 NIGCTPEFVAPELVNVEPLGLDMDMSIGVITYILLGASPELGDFTQKQETLANITSVSD 235
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
194 EIMGTPEYLAPELLNYDPITATDMNNGIITAMVLLHTHTSPFGEQNDQETVINTISOVAVD 253
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
236 FDEEFSSHTELANDKFIKRLLVKETRRKRLTQEALRNHWITPPVD 279
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
254 YSEMFSSVQLATDFDIQSLLVKNPKRPRTESSCLSHMWLOQMD 297

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RESULT      8
T13931
projectin - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13931
R:Daley, J.: Southgate, R.; Ayme-Southgate, A.
J. Mol. Biol. 279, 201-210, 1998
A:Title: Structure of the Drosophila projectin protein: Isoforms and implication for
A:Reference number: z17815; MUID:98300339
A:Accession: T13931
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6658 <DAL>
A:Cross-References: EMBL:AF047475; NID:g3337430; PID:g3337431; PIDN:AAC27550.1
C:Genetics:
A:Gene: projectin
A:Cross-References: FlyBase:FBgn005666
A:Map position: 4
A:Note: Intron positions not resolved (Incomplete sequence)
C:Keywords: muscle

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[illegible]

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Db 5821 EGIHMHQNIILHLDIKPENIMQOTRS--STNVKLIDFGLATRLDPENVYKITTTGAERG 5878
Oy 185 ABEIYVNEPGLGEADMSIGVITYILLSCASPLFGTKQETLANITSVSYDDEEFFSH 244
Db 5879 ABEIYVNEPGLGEADMSIGVITYILLSCASPLFGTKQETLANITSVSYDDEEFFSH 244
Oy 245 SELAKDFIKLLVETKRTKLTIOEALRHPWIPVDN--QOAMVRRSVNLNEMFRQOYR 302
Db 5939 SEAKDFIKLLVETKRTKLTIOEALRHPWIPVDN--QOAMVRRSVNLNEMFRQOYR 302
Oy 303 -RRWKLFSIVSLCNHLTRSLMKK 325
Db 5999 FERFLPIGRLSYSLSRLKLEK 6022

RESULT 9
549128
twitclhn-like protein - California sea hare (fragment)
C:Species: Aplysia californica (California sea hare)
C:Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 17-Nov-2000
C:Accession: S49128; A53923
R:Heierhorst, J.; Probst, W.C.; Vilim, F.S.; Buku, A.; Weiss, K.R.
submitted to the EMBL Data Library, February 1994
A:Description: Autophosphorylation of molluscan twitclhn and interaction of its kinase
A:Reference number: S49128
A:Accession: S49128
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-451 <HE1>
A:Cross-references: EMBL:Z30161; NID:9509412; PIDN:CAA82911.1; PID:9509413
R:Heierhorst, J.; Probst, W.C.; Vilim, F.S.; Buku, A.; Weiss, K.R.
J. Biol. Chem. 269, 21086-21093, 1994
A:Title: Autophosphorylation of molluscan twitclhn and interaction of its kinase domain
A:Reference number: A53923; MUID:94342273
A:Accession: A53923
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 5-372 <HE2>
A:Cross-references: GB:230161
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP
F:45-302/Domain: protein kinase ATP-binding motif
F:53-61/Region: protein kinase ATP-binding motif

Query Match 33.7%; Score 621.5; DB 2; Length 451;
Best Local Similarity 46.0%; Pred. No. 2.6e-19;
Matches 125; Conservative 50; Mismatches 88; Indels 9; Gaps 3;

Oy 5 KOOKVEDPFDIGBELSGGFATVKKCREKSTGLEVAAPFKRKQSRASRGVREIEEIR 64
Db 39 KQSGCDYDIDLEELSGAFGVVHRCVKAATGVEFAKFIN-----TPPLDKYVKN 92
Oy 65 VSILROVLHNHYITLADVENRTDVVHILELVSGELPDLAOKR-SLSEEAATSPFIK 123
Db 93 ISIMQDLNHPKILNCHADAREKDYDLLELFGSLGELPDRIMAEEDYKMSAEVITNMRQA 152
Oy 124 LQGVNLTHTKKTALHPDLKENTMLDKNIPRIKILIDGLAHEIDGVEFKKIFSTPE 183
Db 153 CEGKLHMHHSIVHLDIKPEINMCEYK--ASSVKIIDFGLATKLPDELIVKVTATAE 210
Oy 184 VAPETVNEPGLGEADMSIGVITYILLSCASPLFGTKQETLANITSVSYDDEEFFSH 243
Db 211 ABEIYVNEPGLGEADMSIGVITYILLSCASPLFGTKQETLANITSVSYDDEEFFSH 243
Oy 244 TSELAKDFIKLLVETKRTKLTIOEALRHPW 275
Db 271 VSEAKDFIKLLVETKRTKLTIOEALRHPW 302

RESULT 10
A55021
myosin-light-chain kinase (EC 2.7.1.117), skeletal muscle - rabbit

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C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 24-Sep-1999
C:Accession: A35021; A05120; A25830
R:Heierhorst, J.; Probst, W.C.; Vilim, F.S.; Buku, A.; Weiss, K.R.
J. Biol. Chem. 265, 1724-1730, 1990
A:Title: Domain characterization of rabbit skeletal muscle myosin light chain kinase
A:Reference number: A35021; MUID:90110242
A:Accession: A35021
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-608 <HER>
A:Cross-references: GB:J05194; NID:9165505; PIDN:AAA31400.1; PID:9165506
R:Takio, K.; Blumenthal, D.K.; Edelman, A.M.; Walsh, K.A.; Krebs, E.G.; Titani, K.
Biochemistry 24, 6028-6037, 1985
A:Title: Amino acid sequence of an active fragment of rabbit skeletal muscle myosin
A:Reference number: A05120; MUID:86104095
A:Accession: A05120
A:Molecule type: protein
A:Residues: 237-604 <TRK>
R:Takio, K.; Blumenthal, D.K.; Walsh, K.A.; Titani, K.; Krebs, E.G.
Biochemistry 25, 8049-8057, 1986
A:Title: Amino acid sequence of rabbit skeletal muscle myosin light chain kinase
A:Reference number: A25830; MUID:87101105
A:Accession: A25830
A:Molecule type: protein
A:Residues: 2-336, 'K', 337-604 <TA2>
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; muscle; phosphotransferase; serine/threonine-specific protein kinase
F:595-552/Domain: protein kinase homology <KIN>
F:303-311/Region: protein kinase ATP-binding motif

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Query Match 32.8%; Score 605; DB 2; Length 608;
Best Local Similarity 40.4%; Pred. No. 1.6e-18;
Matches 124; Conservative 63; Mismatches 106; Indels 14; Gaps 5;

Oy 17 EELSGGFATVKKCREKSTGLEVAAPFKRKQSRASRGVREIEEIRVSLROVLHN 76
Db 301 EALGGKFGAVCTCTEKSTGLKLAAYIKOTK-----DKEMYLEIVMQLNHRNL 354
Oy 77 ITLHDVYENRTDVVHILELVSGELPDLAOKR-SLSEEAATSPFIK 135
Db 355 IQLYAAETPHEIIVLEFVEYIEGGELEFRIYDEVDHILEVTDMFVQRICDGIIFMHMRV 414
Oy 136 AHFDIKPENIMLDKNIPRIKILIDGLAHEIDGVEFKKIFSTPEFVAPETVNEP 195
Db 415 LHLIDKPEINLCVNTGHL--VRIIDGLARRYNPNKELKVNFGTPEFLSPEVAVNDQIS 472
Oy 196 LEADMSIGVITYILLSCASPLFGTKQETLANITSVSYDDEEFFSHSELAKDFIK 255
Db 473 DKTDMSLGVITYILLSCASPLFGTKQETLANITSVSYDDEEFFSHSELAKDFIK 255
Oy 256 LKVEKRTKLTIOEALRHPWIPVDNQAMVR--ESVVLNENFRKOYVRRWKLFS 313
Db 533 IVEQGRMSAQAOLAPWLNLEAKKRCNRLKSGILL--KKYLKMRMKKNFTAVS 589
Oy 314 LCNHLTR 320
Db 590 AANRFKK 596

RESULT 11
A28798
myosin-light-chain kinase (EC 2.7.1.117), skeletal muscle - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jan-1989 #sequence_revision 12-Jan-1989 #text_change 19-Dec-1997
C:Accession: A28798; A60441
R:Roush, C.L.; Kennelly, P.J.; Giacomini, M.B.; Helman, D.M.; Scott, J.D.; Krebs, E.G.
J. Biol. Chem. 263, 10510-10516, 1988
A:Title: Isolation of the cDNA encoding rat skeletal muscle myosin light chain kinase
A:Reference number: A28798; MUID:88273159
A:Accession: A28798
A:Molecule type: mRNA

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Query Match	32.7%;	Score 604;	DB 2;	Length 610;
Best Local Similarity	39.1%;	Pred. No. 1.8e-18;		
Matches 120;	Conservative 67;	Mismatches 106;	Indels 14;	Gaps 5;

RESULT 12

1,7522
 hypothetical protein ZC373.4 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C:Accession: J27522
 R:Kershaw, J.
 submitted to the EMBL Data Library, April 1995
 A:Reference number: Z20382
 A:Accession: J27522
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1211 <WIL>
 A:Cross-references: EMBL:Z49131; PIDN:CMA88976.1; GSPDB:GN00028; CESP:ZC373.4
 A:Experimental source: clone ZC373
 C:Genetics:
 A:Gene: CESP:ZC373.4
 A:Map position: X
 A:Introns: 20/1; 53/2; 80/3; 122/2; 169/3; 198/3; 236/2; 286/2; 337/3; 381/3; 402/3; 445/3

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Query Match 31.9%; Score 589; DB 2; Length 1211;
Best Local Similarity 41.2%; Pred. No. 1.4e-17;
Matches 140; Conservative 48; Mismatches 112; Indels 40; Gaps 8;

QY      8 KVEDFYDIGELSGGQFAFYKKCRESTGIEFYAKTIKKRQASASRGVSREIEEVS 67
      - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Db 40 KPLTLYQVNTLLDDGKRGKVCVIEETGSEFAKTIK-----IKKRDRAVEEVS 93

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OY      68 LROVLHNVTLLADV - YENKTDVYHITELVSGELDEFLAOKE - SLSEBATSFIKOIND 125
Db      94 LTOHRHRIQIYAFATTTNDVLLIMELVSGELDEPRVAEESYVSELAIVMIICOLE 153
OY      126 GVNLTHPRKIAHFDKPEINIMLLDKNIPRIHKLIDFGALHIEDGVEEKNIFGTPEFA 185
Db      154 AIDYIHKNMILHLDVCKENICMV - SLTGNRIRKIDBLGRALRHVDGQOELVYMGATEEFA 211
OY      186 PEIYVNEPFLGLEADWMSIGVYTYLLSGASPELDGTQOETLANITSVYDFDEEFESH 245
Db      212 PEVIKFEELDYHTWMSIGVYTYLLLSGSPFLSDNIGETVCANVEKGVMEFTEEDPVT 271
OY      246 ELAKDFELKLIVKETRRKRLTIOELRHPWT-----PVNQOAMVR 286
Db      272 E-AKDFEVLKLLVDOOSKRMLRHELODHPWIAKHROKAAACNTILEKPLNADLTOKQIM-- 328
OY      287 RESVYNLENFRKQYRRWKLTSFSLVSLCNHLTSLAKKV 326
Db      329 -----RYNARKKE--RRLIYVFLIMNRLNRSLSTRM 360

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RESULT      13
A88852
protein unc-22 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: A88852
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio
A:Reference number: A75000; MUID:99065613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C-
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
A:Accession: A88852
A:status: preliminary
A:Molecule type: DNA
A:Residues: 1-6831 <STO>
A:Cross references: GB:chr_IV; PIDN:CA98081.1; PID:g3881830; GSFDB:GN00022
C:genetics:
A:gene: unc-22
A:map position: 4
C:Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homolog

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Query Match	31.7%	Score 584.5	DB 2	Length 6831
Best Local Similarity	42.0%	Pred. No. 1e-16	98	Indels 9
Matches 115	Conservative 52	Mismatches		Gaps 3
Qy	5	KOCQVEDFYUIGELSGSGFAIVKCKCEKSTGLETAAKFTKKQSRASRGVSRELERE	64	
Db	5926	KHDVLDHDIHDELSTGAGGVNHRVTERATGNNFAKFWPTDHE- - - - -DKETVKE	5979	
Qy	65	VSILKQVLIHNVITLHUYENRDTNVIIELSGGELFDLADKES-TSEEAATSEFIKOI	123	
Db	5980	IQTMSVLIHPLVLIHDAFEDDNEVMNVIIEFMSSGELFEKLVADQHNKMSDEALVEAVMROV	6039	
Qy	124	LDGVNVLHTTKIAHFDLKPENIMILDKNIPRIYAKLIDFGLADHEIDGVSEFKNIFGPRF	183	
Db	6040	CKSGCIHMENNVYHDLKRPENIMFTTKR--SNEKLKIDFGLADHLDKQSVAKYTTGTAER	6097	
Qy	184	VAPELVNVREGLBADMSISGIVYIILSGASPLDGTOKETLANITSVSYDDEEFFSH	243	
Db	6098	AAPEVAEKKRPGLYTTDMMSVGLSYIILSGLSPRGGENDETLRNKVSCDMMDSAFSG	6157	
Qy	244	TSELAKDFIRKLVLKETRKRLITIOELALRHPIYTP	277	
Db	6158	ISEDGKDFIRKLVLADPNTKMTIQAQLEHNPULIP	6191	

RESULT 14
557242
twitchin [similarity] - Caenorhabditis elegans

N: Alternate names: myosin-regulating protein
 N: Contains: protein kinase (EC 2.7.1.1-)
 C: Species: *Caenorhabditis elegans*
 C: Date: 28-Oct-1995 #sequence-revision 24-Oct-1997 #text-change 20-Jun-2000
 C: Accession: S57242; S07571; S06797; S57218; T27934; T28030
 R: Benlian, G.M.; L'Hernault, S.W.; Morris, M.E.
 submitted to the EMBL Data Library, February 1993
 A: Description: Additional sequence complexity within twitching of *Caenorhabditis elegans*
 A: Reference number: S57242
 A: Accession: S57242
 A: Molecule type: DNA
 A: Residues: 1-683 <BEN1>
 A: Cross-references: EMBL: L10351
 A: Experimental source: var. Bristol
 R: Benlian, G.
 submitted to the EMBL Data Library, November 1989
 A: Reference number: S07571
 A: Accession: S07571
 A: Molecule type: DNA
 A: Residues: 792-6839 <BEN2>
 A: Cross-references: EMBL: X15423; NID: g6897; PIDN: CAA33463.1; PID: g6898
 A: Experimental source: var. Bristol
 R: Benlian, G.M.; Kilt, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, R.H.
 Nature 342, 45-50, 1989
 A: Title: Sequence of an unusually large protein implicated in regulation of myosin activity
 A: Reference number: S06797; MUID: 90044042
 A: Accession: S06797
 A: Status: nucleic acid sequence not shown
 A: Molecule type: DNA
 A: Residues: 806-1175; 1178-1998, 'Y', 2000-3040, 'I', 3042-3335, 'I', 3337-5693; 5696-6359, 'I', 6361-6363
 A: Cross-references: EMBL: X15423
 A: Experimental source: var. Bristol
 R: Benlian, G.M.; L'Hernault, S.W.; Morris, M.E.
 Genetics 134, 1097-1104, 1993
 A: Title: Additional sequence complexity in the muscle gene, unc-22, and its encoded product
 A: Reference number: S57218; MUID: 93387664
 A: Accession: S57218
 A: Molecule type: DNA
 A: Residues: 2-99; 108-194, 'O', 196-206; 374-468; 658-753 <BEN4>
 A: Experimental source: var. Bristol
 R: White, S.
 submitted to the EMBL Data Library, May 1996
 A: Reference number: Z20442
 A: Accession: T27934
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: MGIPGKKCKO', 19-6839 <WIL>
 A: Cross-references: EMBL: Z73897; PIDN: CAA98064.1; GSPDB: GN00022; CESP: ZK617.1a
 A: Experimental source: clone ZK617
 R: Harris, B.
 submitted to the EMBL Data Library, May 1996
 A: Reference number: Z20458
 A: Accession: T28030
 A: Status: preliminary; translated from GB/EMBL/DBJ
 A: Molecule type: DNA
 A: Residues: 'MGIPGKKCKO', 19-6839 <WIL2>
 A: Cross-references: EMBL: Z73899; PIDN: CAA98081.1; GSPDB: GN00022; CESP: ZK617.1a
 A: Experimental source: clone ZK829
 C: Comment: Lack of unc-22 leads to a constant twitching of the body muscles.
 C: Genetics:
 A: Gene: unc-22; CESP: ZK617.1a
 A: Map position: 4
 A: Introns: 18/3; 69/3; 143/2; 176/3; 264/2; 387/3; 413/2; 471/1; 516/3; 550/3; 582/3; 60152/3; 6691/3; 6776/1; 6808/3
 C: Superfamily: twitchin; fibronectin type III repeat homology; immunoglobulin homology;
 C: Keywords: ATP; autophosphorylation; duplication; muscle; phosphotransferase; serine/threonine kinase
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